

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=1; day=6; hr=15; min=23; sec=26; ms=293;]

=====

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=1; day=6; hr=15; min=19; sec=30; ms=812;]

=====

Application No: 10540394 Version No: 3.0

Input Set:

Output Set:

Started: 2009-12-17 16:24:08.581
Finished: 2009-12-17 16:24:11.528
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 947 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 25
Actual SeqID Count: 25

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2009-12-17 16:24:08.581
Finished: 2009-12-17 16:24:11.528
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 947 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 25
Actual SeqID Count: 25

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)

SUBSTITUTE SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> Novel protein and its use

<130> 3132WOOP

<140> 10540394

<141> 2005-09-01

<150> JP2002-378052

<151> 2002-12-26

<150> JP2003-65497

<151> 2003-03-11

<160> 25

<210> 1

<211> 837

<212> PRT

<213> Human

<400> 1

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
5 10 15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu
20 25 30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
35 40 45
Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
50 55 60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65 70 75 80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
85 90 95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
100 105 110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
115 120 125
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
130 135 140
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145 150 155 160
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
165 170 175
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
180 185 190
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
195 200 205
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
210 215 220
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225 230 235 240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
245 250 255

Asp Asp Lys Ile Tyr Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
260 265 270
Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
275 280 285
Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
290 295 300
Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305 310 315 320
Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
325 330 335
Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
340 345 350
Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
355 360 365
Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Met
370 375 380
Val His Arg Asp Pro Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385 390 395 400
Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
405 410 415
Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
420 425 430
Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
435 440 445
Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
450 455 460
Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465 470 475 480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
485 490 495
Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
500 505 510
Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
515 520 525
Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
530 535 540
Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545 550 555 560
Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
565 570 575
Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
580 585 590
Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
595 600 605
Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
610 615 620
Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625 630 635 640
Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
645 650 655
Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
660 665 670
Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
675 680 685
Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
690 695 700
Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val

705	710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe Leu		
725	730	735	
Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu			
740	745	750	
Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu			
755	760	765	
Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His			
770	775	780	
Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe			
785	790	795	800
Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu			
805	810	815	
Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile			
820	825	830	
Arg Asp Ser Val Val			
	835		

<210> 2
<211> 2511
<212> DNA
<213> Human

<400> 2

atgctgcgca ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg	60
cctcggccac cgctgtctgt ctgcgtgtcc tgctgcagcc gcccgttccg	120
acctgggcgc tcagcccccg gatcagccctg cctctggct ctgaagagcg gccatttcctc	180
agattcgaag ctgaacacat ctccaactac acagcccttc tgctgagcag ggatggcagg	240
accctgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagttctcg	300
ccaggcgggg agtaccagga gctgcttg gggtgcagacg cagagaagaa acagcagtgc	360
agcttcaagg gcaaggaccc acagcgcgac tgtcaaaaact acatcaagat ctcctgtccg	420
ctcagcggca gtcacctgtt cacctgtggc acagcagcct tcagcccat gtgtacctac	480
atcaacatgg agaacttcac cctggcaagg gacgagaagg ggaatgtcct cctggaaagat	540
ggcaaggggcc gttgtccctt cgacccgaat ttcaagtcca ctgcccgtt gttgtatggc	600
gagctctaca ctggaacagt cagcagcttc caagggaatg acccgccat ctgcggagc	660
caaagccttc gccccaccaa gaccgagac tccctcaact ggctgcaaga cccagcttt	720
gtggcctcag ctcacattcc tgagagccctg ggcagcttc aaggcgatga tgacaagatc	780
tacttttct tcagcgagac tggccaggaa tttgagttct ttgagaacac cattgtgtcc	840
cgcattgccc gcatctgcaa gggcgatgag ggtggagagc gggtgctaca gcagcgctgg	900
acctccttcc tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac	960
gtgctgcagg atgtttcac gtcgagcccc agccccagg actggcgtga cacccttttc	1020
tatgggtct tcactttcca gtggcacagg ggaactacag aaggctctgc cgtctgtgtc	1080
ttcacaatga aggatgtgca gagagtcttc agcggctct acaaggaggt gaaccgtgag	1140
acacagcaga tggcaccccg tgacccaccc gtgcccacac cccggcctgg agcgtgcata	1200
accaacagtg cccggaaag gaagatcaac tcatccctgc agctcccaga cccggtgtcg	1260
aactttctca aggaccattt cctgatggac gggcagggtcc gaagccgcat gtcgtgtcg	1320
cagccccagg ctgcgtacca ggcgtggct gtacaccggc tccctggct gcaccacacc	1380
tacgatgtcc tcttcgtgg cactgggtac ggccggctcc acaaggcagt gagcgtggc	1440
ccccgggtgc acatcattga ggagctgcag atcttctcat cgggacagcc cgtgcagaat	1500
ctgctcctgg acaccacag ggggtgtctg tatgcggcct cacactcggt cgtagtccag	1560
gtgcccattgg ccaactgcag cctgtaccgg agctgtgggg actgcctcct cggccggagc	1620
ccctactgtg ctggagccg ctccagctgc aagcacgtca gcctctacca gcctcagctg	1680
gccaccaggc cgtggatcca ggacatcgag ggagccagcg ccaaggacct ttgcagcgcg	1740
tcttcgggtt tgcggcgtt tttgtacca acaggggaga agccatgtga gcaagtccag	1800
ttccagccca acacagtgaa cactttggcc tgccgcgtcc tctccaaacct ggccgacccga	1860
ctctggctac gcaacggggc ccccgtaat gcctggcct cctgccacgt gtcaccact	1920

ggggacctgc	tgctggtggg	cacccaacag	ctggggaggt	tccagtgtcg	gtcaactagag	1980
gagggcttcc	agcagctgtt	agccagctac	tgcccagagg	tggtggagga	cggggtgtggca	2040
gaccaaacag	atgagggtgg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctggtg	gcaaggccag	ctggggtgca	gacaggtcct	actggaagga	gttcctggtg	2160
atgtgcacgc	tctttgtgt	ggccgtgtcg	ctcccaagttt	tattcttgct	ctaccggcac	2220
cggAACAGCA	tgaaagtctt	cctgaagcag	gggaaatgtg	ccagcgtgca	ccccaaagacc	2280
tgccctgtgg	tgctggcccc	tgagacccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggta	ccagtccctg	tcagacagcc	ccccggggtc	ccgagtttcc	2400
actgagtca	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgccccccggc	cccggtcccg	ccttggctcg	gagatccgtg	actctgtgg	g	2511

<210> 3
<211> 3766
<212> DNA
<213> Human

<400> 3

gctctgccc	agccgaggct	gcggggccgg	cgccggcg	aggactgcgg	tgccccgcgg	60
aggggctgag	tttgcacggg	cccaacttgc	cctgtttccc	acctccgc	ccccagggtcc	120
ggaggcg	gccccgggg	cgactcg	gggg	gcggaccgcg	ggggcgagct	180
agtccggcc	agccacactg	gccc	gagccg	cgggacaccg	tcgtcttgc	240
ctgcgcaccc	cgatgggc	cttggagctgg	ctcgccgccc	catggggcgc	gctgccgcct	300
cggccaccgc	tgctgtgt	cctgtgtgt	ctgtcttgc	tgagcgcgc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggcctgt	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgtcgaga	ggcccttctt	gcactcagta	gcaacctcag	cttcctgc	540
ggcggggagt	accaggagct	gttttgggt	gcagacgcag	agaagaaaaca	gcagtgc	600
ttcaaggc	aggacccaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgcgc	660
agcggcagtc	acctgttac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttccaccc	ggcaagggac	gagaaggg	atgtcccttgc	ggaagatggc	780
aaggggcgtt	gtcccttcga	cccgaaattt	aagtccactg	ccctgggtgg	tgtggcag	840
ctctacactg	gaacagtc	cagcttccaa	gggaatgacc	cgcccatctc	gcggagccaa	900
agccttcg	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agctttgtg	960
gcctcagc	acattcctga	gagcctggc	agcttgca	gcgtatgat	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttcttgc	agaacaccat	tgtgtccgc	1080
attggccgca	tctgc	aaagggt	cgatgggg	ggagagcggg	tgctacagca	1140
tccttcctca	aggccagct	gtgtgtc	cgccccgac	atggcttccc	cttcaacgt	1200
ctgcaggatg	tcttacgc	gagcccc	ccccaggact	ggcgtgacac	ccttttat	1260
ggggcttca	cttccc	actgtgg	gcacagg	actacagaag	gctctgttgc	1320
acaatgaagg	atgtcagag	acttcc	cgacgg	aggaggtgaa	ccgtgagaca	1380
cagcagatgg	tacaccgt	ccca	cccc	ggcgtgg	gtgc	1440
aacagtgc	gggaaaggaa	gatcaact	tccctgc	ccccc	cg	1500
tttctcaagg	accacttct	gatggacgg	cagg	gttgc	gtc	1560
ccccagg	gctacc	cg	ccgt	ccat	cc	1620
gatgtct	tcctgg	tggt	ggc	gttgc	ccat	1680
cgggtgcaca	tcatt	gagga	gtc	gac	ccat	1740
ctcctggaca	cccac	agg	gtc	gttgc	ccat	1800
ccatggcca	actgc	agg	gtc	ccat	ccat	1860
tactgtgtt	ggagcgg	cag	gtc	ccat	ccat	1920
accaggccgt	ggatcc	agg	gtc	ccat	ccat	1980
tcgggtgt	ccccgtt	tgt	acc	ccat	ccat	2040
cagcccaaca	cagt	gaa	ccg	ccat	ccat	2100
tggctacgca	acgggg	cgt	cc	ccat	ccat	2160
gacctgtgc	tgg	ggc	cc	ccat	ccat	2220
ggcttcc	ccat	ggc	cc	ccat	ccat	2280
caaacagatg	agg	gttgc	ccat	ccat	ccat	2340

gctggtggca	aggccagctg	gggtgcagac	aggtcctact	ggaaggagtt	cctggtgatg	2400
tgcacgctct	ttgtgctggc	cgtgctgctc	ccagtttat	tcttgctcta	ccggcacccgg	2460
aacagcatga	aagtcttcct	gaagcagggg	gaatgtgcca	gcgtgcaccc	caagacctgc	2520
cctgtggtgc	tgccccctga	gaccggccca	ctcaacggcc	tagggcccccc	tagcaccacca	2580
ctcgatcacc	gagggtacca	gtccctgtca	gacagcccc	cggggtccc	agtcttact	2640
gagtcagaga	agaggccact	cagcatccaa	gacagctcg	tggaggtatc	cccagtgtgc	2700
ccccggcccc	gggtccgcct	tggctcgag	atccgtact	ctgtggtgtg	agagctgact	2760
tccagaggac	gtgccttgg	cttcaggggc	tgtgaatgct	cggagagggt	caactggacc	2820
tcccccctccgc	tctgctcttc	gtggaacacg	accgtggtgc	ccggcccttg	ggagccttgg	2880
ggccagctgg	cctgctgctc	tccagtcaag	tagcgaagct	cctaccaccc	agacacccaa	2940
acagccgtgg	ccccagaggt	cctggccaaa	tatggggcc	tgccttaggtt	ggtgaaacag	3000
tgctccttat	gtaaaactgag	ccctttgttt	aaaaaaacaat	tccaaatgtg	aaactagaat	3060
gagagggaaag	agatagcatg	gcatgcagca	cacacggctg	ctccagtta	tggcctccca	3120
gggggtctgg	ggatgcatcc	aaagtggttt	tctgagacag	agttggaaac	cctcaccacac	3180
tggccttcc	accttccaca	ttatcccgt	gccaccggct	gccctgtctc	actgcagatt	3240
caggaccagc	ttgggctgcg	tgcgttctgc	cttgcagtc	agccgaggat	gtagttgtt	3300
ctgcccgtgt	cccaccacct	cagggaccag	aggcttaggt	tggcactgcg	gccctcacca	3360
ggtcctgggc	tccggcccaa	ctcctggacc	tttccagcct	gtatcaggct	gtggccacac	3420
gagaggacag	cgcgagctca	ggagagattt	cgtgacaatg	tacgccttcc	cctcagaatt	3480
cagggaaagag	actgtcgct	gccttcctcc	gttgttgcgt	gagaacccgt	gtgcccccttc	3540
ccaccatatc	caccctcgct	ccatctttga	actcaaacac	gaggaactaa	ctgcaccctg	3600
gtcctctccc	cagtccccag	ttcacccctcc	atccctcacc	ttcctccact	ctaaggata	3660
tcaacactgc	ccagcacagg	ggccctgaat	ttatgtggtt	tttatacatt	tttaataag	3720
atgcacttta	tgtcattttt	taataaaagtc	tgaagaatta	ctgttt		3766

<210> 4

<211> 837

<212> PRT

<213> Human

<400> 4

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro	Trp
					5				10					15	
Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu							
								20		25				30	
Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	Pro	Arg	Ile
								35		40				45	
Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu	Arg	Phe	Glu	Ala
						50		55		60					
Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu	Ser	Arg	Asp	Gly	Arg
						65		70		75					80
Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu	Phe	Ala	Leu	Ser	Ser	Asn
						85		90						95	
Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr	Gln	Glu	Leu	Leu	Trp	Gly	Ala
						100		105						110	
Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys	Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln
						115		120						125	
Arg	Asp	Cys	Gln	Asn	Tyr	Ile	Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser
						130		135		140					
His	Leu	Phe	Thr	Cys	Gly	Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr
						145		150		155					160
Ile	Asn	Met	Glu	Asn	Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val
						165		170						175	
Leu	Leu	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys
						180		185						190	
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ile

195	200	205
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg		
210	215	220
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe		
225	230	235
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp		
245	250	255
Asp Asp Lys Ile Tyr Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu		
260	265	270
Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly		
275	280	285
Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu		
290	295	300
Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn		
305	310	315
Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg		
325	330	

SUBSTITUTE SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> Novel protein and its use

<130> 3132WOOP

<140> 10540394

<141> 2005-09-01

<150> JP2002-378052

<151> 2002-12-26

<150> JP2003-65497

<151> 2003-03-11

<160> 25

<210> 1

<211> 837

<212> PRT

<213> Human

<400> 1

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro Trp
5 10 15
Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu Leu
20 25 30
Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser Pro Arg Ile
35 40 45
Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu Arg Phe Glu Ala
50 55 60
Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu Ser Arg Asp Gly Arg
65 70 75 80
Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Leu Ser Ser Asn
85 90 95
Leu Ser Phe Leu Pro Gly Gly Glu Tyr Gln Glu Leu Leu Trp Gly Ala
100 105 110
Asp Ala Glu Lys Lys Gln Gln Cys Ser Phe Lys Gly Lys Asp Pro Gln
115 120 125
Arg Asp Cys Gln Asn Tyr Ile Lys Ile Leu Leu Pro Leu Ser Gly Ser
130 135 140
His Leu Phe Thr Cys Gly Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr
145 150 155 160
Ile Asn Met Glu Asn Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val
165 170 175
Leu Leu Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys
180 185 190
Ser Thr Ala Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser
195 200 205
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg
210 215 220
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
225 230 235 240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp
245 250 255

Asp Asp Lys Ile Tyr Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu
260 265 270
Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly
275 280 285
Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu
290 295 300
Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn
305 310 315 320
Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg
325 330 335
Asp Thr Leu Phe Tyr Gly Val Phe Thr Ser Gln Trp His Arg Gly Thr
340 345 350
Thr Glu Gly Ser Ala Val Cys Val Phe Thr Met Lys Asp Val Gln Arg
355 360 365
Val Phe Ser Gly Leu Tyr Lys Glu Val Asn Arg Glu Thr Gln Gln Met
370 375 380
Val His Arg Asp Pro Pro Val Pro Thr Pro Arg Pro Gly Ala Cys Ile
385 390 395 400
Thr Asn Ser Ala Arg Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro
405 410 415
Asp Arg Val Leu Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln
420 425 430
Val Arg Ser Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg
435 440 445
Val Ala Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu
450 455 460
Phe Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
465 470 475 480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly Gln
485 490 495
Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu Tyr Ala
500 505 510
Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn Cys Ser Leu
515 520 525
Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala
530 535 540
Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu Tyr Gln Pro Gln Leu
545 550 555 560
Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu Gly Ala Ser Ala Lys Asp
565 570 575
Leu Cys Ser Ala Ser Ser Val Val Ser Pro Ser Phe Val Pro Thr Gly
580 585 590
Glu Lys Pro Cys Glu Gln Val Gln Phe Gln Pro Asn Thr Val Asn Thr
595 600 605
Leu Ala Cys Pro Leu Leu Ser Asn Leu Ala Thr Arg Leu Trp Leu Arg
610 615 620
Asn Gly Ala Pro Val Asn Ala Ser Ala Ser Cys His Val Leu Pro Thr
625 630 635 640
Gly Asp Leu Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys
645 650 655
Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro
660 665 670
Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser
675 680 685
Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly
690 695 700
Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val

705	710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe Leu		
725	730	735	
Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu			
740	745	750	
Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu			
755	760	765	
Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His			
770	775	780	
Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ser Arg Val Phe			
785	790	795	800
Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu			
805	810	815	
Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile			
820	825	830	
Arg Asp Ser Val Val			
835			

<210> 2
<211> 2511
<212> DNA
<213> Human

<400> 2

atgctgcgca ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg	60
cctcggccac cgctgtctgt ctgcgtgtcc tgctgcagcc gcccgttcc	120
acctgggcgc tcagcccccg gatcagccctg cctctggct ctgaagagcg gccatttc	180
agattcgaag ctgaacacat ctccaactac acagcccttc tgctgagcag ggatggcagg	240
accctgtacg tgggtgctcg agaggccctc tttgcactca gtagcaacct cagttctcg	300
ccaggcgggg agtaccagga gctgcttg gggtgcagacg cagagaagaa acagcagtgc	360
agcttcaagg gcaaggaccc acagcgcgac tgtcaaaaact acatcaagat ctcctgtcc	420
ctcagcggca gtcacctgtt cacctgtggc acagcagcc tcaagcccat gtgtacccat	480
atcaacatgg agaacttcac cctggcaagg gacgagaagg ggaatgtcct cctggaaagat	540
ggcaaggggcc gttgtccctt cgacccgaat ttcaagtcca ctgcccgtt ggttcatggc	600
gagctctaca ctggaacagt cagcagcttc caagggaatg acccgccat ctgcggagc	660
caaagccttc gccccaccaa gaccgagac tccctcaact ggctgcaaga cccagcttt	720
gtggcctcag ctcacattcc tgagagccctg ggcagcttc aaggcgatga tgacaagatc	780
tacttttct tcagcgagac tggccaggaa tttgagttct ttgagaacac cattgtgtcc	840
cgcattgccc gcatctgcaa gggcgatgag ggtggagagc gggtgctaca gcagcgctgg	900
acctccttcc tcaaggccca gctgctgtgc tcacggcccg acgtggctt ccccttcaac	960
gtgctgcagg atgtttcac gtcgagcccc agccccagg actggcgtga cacccttttc	1020
tatgggtct tcactttcca gtggcacagg ggaactacag aaggctctgc cgtctgtgtc	1080
ttcacaatga aggatgtgca gagagtcttc agcggctct acaaggaggt gaaccgtgag	1140
acacagcaga tggcaccccg tgacccaccc gtgcccacac cccggcctgg agcgtgcata	1200
accaacagtg cccggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgtc	1260
aactttctca aggaccattt cctgatggac gggcagggtcc gaagccgcat gtcgtgtc	1320
cagccccagg ctgcgtacca ggcgtggct gtacaccgg tccctggct gcaccacacc	1380
tacgatgtcc tcttcgtgg cactgggtac ggccggctcc acaaggcagt gagcgtggc	1440
ccccgggtgc acatcattga ggagctgcag atcttctcat cgggacagcc cgtgcagaat	1500
ctgctcctgg acaccacag ggggtgtctg tatgcggcct cacactcggt cgtagtccag	1560
gtgcccgtt ccaactgcag cctgtaccgg agctgtgggg actgcctcct cggccggac	1620
ccctactgtg ctggagccg ctccagctgc aagcacgtca gcctctacca gcctcagctg	1680
gccaccaggc cgtggatcca ggacatcgag ggagccagcg ccaaggaccc ttgcagcgc	1740
tcttcgggtt tgtccccgtc tttgtacca acaggggaga agccatgtga gcaagtccag	1800
ttccagccca acacagtgaa cactttggcc tgcccgctcc tctccaaacct ggccgacccga	1860
ctctggctac gcaacggggc ccccgtaat gcctggctt cctgccacgt gtcaccact	1920

ggggacctgc	tgctggtggg	cacccaacag	ctggggaggt	tccagtgtcg	gtcaactagag	1980
gagggcttcc	agcagctgtt	agccagctac	tgcccagagg	tggtggagga	cggggtgtggca	2040
gaccaaacag	atgagggtgg	cagtgtaccc	gtcattatca	gcacatcgcg	tgtgagtgca	2100
ccagctgggt	gcaaggccag	ctgggggtca	gacaggtcct	actggaagga	gttcctgggt	2160
atgtgcacgc	tctttgtgt	ggccgtgtcg	ctcccaagttt	tattcttgct	ctaccggcac	2220
cggAACAGCA	tgaaagtctt	cctgaagcag	gggaaatgtg	ccagcgtgca	ccccaaagacc	2280
tgccctgtgg	tgctggcccc	tgagacccgc	ccactcaacg	gcctagggcc	ccctagcacc	2340
ccactcgatc	accgagggta	ccagtccctg	tcagacagcc	ccccggggtc	ccgagtttcc	2400
actgagtca	agaagaggcc	actcagcatc	caagacagct	tcgtggaggt	atccccagtg	2460
tgccccccggc	cccggtcccg	ccttggctcg	gagatccgtg	actctgtgggt	g	2511

<210> 3

<211> 3766

<212> DNA

<213> Human

<400> 3

gctctgccc	agccgaggct	gcggggccgg	cgccggcg	aggactgcgg	tgccccgcgg	60
aggggctgag	tttgcacggg	cccaacttgc	cctgtttccc	acctccgc	ccccagggtcc	120
ggaggcg	gccccgggg	cgactcg	ggggcaccgc	ggggcgagct	gcccggcg	180
agtccggcc	agccacactg	gcccggaccc	cgggacaccc	tcgtcttgc	tctccgaatg	240
ctgcgcaccc	cgatgggcct	gaggagctgg	ctgcggcccc	catggggcgc	gctggccgc	300
cggccaccgc	tgctgtgt	cctgtgtgt	ctgtcttgc	tgagcggcc	gcctccgacc	360
tgggcgctca	gccccggat	cagcctgcct	ctgggctctg	aagagcggcc	attcctcaga	420
ttcgaagctg	aacacatctc	caactacaca	gcccttctgc	tgagcaggga	tggcaggacc	480
ctgtacgtgg	gtgtcgaga	ggcccttctt	gcactcagta	gcaacctcag	tttgcgttca	540
ggcggggagt	accaggagct	gtttgggg	gcagacgcag	agaagaaaaca	gcagtgcagc	600
ttcaaggcaca	aggacccaca	gcgcgactgt	caaaactaca	tcaagatcct	cctgcccgtc	660
agcggcagtc	acctgttcac	ctgtggcaca	gcagccttca	gccccatgtg	tacctacatc	720
aacatggaga	acttccaccc	ggcaagggac	gagaagggga	atgtccctcc	ggaagatggc	780
aaggggcgtt	gtcccttcga	cccgaaattt	aagtccactg	ccctgggtgg	tgtggcag	840
ctctacactg	gaacagtcag	cagcttccaa	gggaatgacc	cgcccatctc	gcccggccaa	900
agccttcg	ccaccaagac	cgagagctcc	ctcaactggc	tgcaagaccc	agctttgtg	960
gcctcagcct	acattcctga	gagcctgggc	agcttgcaag	gcgtatgt	caagatctac	1020
tttttcttca	gcgagactgg	ccaggaattt	gagttcttt	agaacaccat	tgtgtccgc	1080
attggccgca	tctgcacggg	cgatgggggt	ggagagcggg	tgctacagca	gcgttggacc	1140
tccttcctca	aggccagct	gtgtgtca	cgcccccacg	atggcttccc	tttcaacgtg	1200
ctgcaggatg	tcttcacgt	gagcccccac	ccccaggact	ggcgtgacac	ccttttctat	1260
ggggcttca	cttcccagtg	gcacagggga	actacagaag	gctctggcg	ctgtgttttca	1320
acaatgaagg	atgtcagag	agtcttcag	ggccttaca	aggaggtgaa	ccgttgcagaca	1380
cagcagatgg	tacaccgt	cccacccgt	cccacacccc	ggcgttggacc	gtgtatcacc	1440
aacagtgc	gggaaaggaa	gatcaactca	tccctgcac	tcccagaccc	cggtgttgcac	1500
tttctcaagg	accacttc	gatggacgg	caggtccgaa	gccgcacgt	gctgtgtcag	1560
ccccaggctc	gctaccagcg	cgtggctgt	caccgcgtcc	ctggcctgca	ccacacccat	1620
gatgtcttct	tcctgggcac	tggtgacgg	cggctccaca	aggcagttag	cgtggccccc	1680
cgggtgcaca	tcatttggg	gtgcagatc	tttgcacccgg	gacagccgt	gcagaatctg	1740
tccttggaca	cccacagggg	gtgtgttat	gcggccctac	actcggcg	agtccaggt	1800
cccatggcca	actgcaccc	gttccggac	tgtggggact	gccttctcg	ccgggacccc	1860
tactgtgtt	ggagcggctc	cagctgca	cacgtcagcc	tctaccagcc	tcagctggcc	1920
accaggccgt	ggatccagga	catcgaggga	gccagcgc	aggacctt	cagcgcgt	1980
tcgggtgtgt	ccccgtt	tgttaccaaca	ggggagaagc	catgtgagca	agtccagttc	2040
cagcccaaca	cagtgaacac	tttggcttc	ccgcttctt	ccaacctggc	gaccgcactc	2100
tggctacgca	acggggcccc	cgtcaatgc	tcggcttctt	gccacgtgt	accactggg	2160
gacctgtgc	tggtgccac	ccaacagctg	ggggagttcc	agtgtgttgc	actagaggag	2220
ggcttccagc	agctgttagc	cagctactgc	ccagaggtgg	tggaggacgg	ggtggcagac	2280
caaacagatg	agggtggcag	tgttccctgc	attatcagca	catcgctgt	gagtgcacca	2340

gctggtggca	aggccagctg	gggtgcagac	aggtcctact	ggaaggagtt	cctggtgatg	2400
tgcacgctct	ttgtgctggc	cgtgctgctc	ccagtttat	tcttgctcta	ccggcacccgg	2460
aacagcatga	aagtcttcct	gaagcagggg	gaatgtgcca	gcgtgcaccc	caagacctgc	2520
cctgtggtgc	tgccccctga	gaccggccca	ctcaacggcc	tagggcccccc	tagcaccacca	2580
ctcgatcacc	gagggtacca	gtccctgtca	gacagcccc	cggggtccc	agtcttact	2640
gagtcagaga	agaggccact	cagcatccaa	gacagctcg	tggaggtatc	cccagtgtgc	2700
ccccggcccc	gggtccgcct	tggctcgag	atccgtact	ctgtggtgtg	agagctgact	2760
tccagaggac	gtgccttgg	cttcaggggc	tgtgaatgct	cggagagggt	caactggacc	2820
tcccccctccgc	tctgctcttc	gtggaacacg	accgtggtgc	ccggcccttg	ggagccttgg	2880
ggccagctgg	cctgctgctc	tccagtcaag	tagcgaagct	cctaccaccc	agacacccaa	2940
acagccgtgg	ccccagaggt	cctggccaaa	tatggggcc	tgccttaggtt	ggtgaaacag	3000
tgctccttat	gtaaaactgag	ccctttgttt	aaaaaaacaat	tccaaatgtg	aaactagaat	3060
gagagggaaag	agatagcatg	gcatgcagca	cacacggctg	ctccagtta	tggcctccca	3120
gggggtctgg	ggatgcatcc	aaagtgggtt	tctgagacag	agttggaaac	cctcaccacac	3180
tggccttcc	accttccaca	ttatcccgt	gccaccggct	gccctgtctc	actgcagatt	3240
caggaccagc	ttgggctgcg	tgcgttctgc	cttgcagtc	agccgaggat	gtagttgtt	3300
ctgcccgtgt	cccaccacct	cagggaccag	aggcttaggt	tggcactgcg	gccctcacca	3360
ggtcctgggc	tccggcccaa	ctcctggacc	tttccagcct	gtatcaggct	gtggccacac	3420
gagaggacag	cgcgagctca	ggagagattt	cgtgacaatg	tacgccttcc	cctcagaatt	3480
cagggaaagag	actgtcgct	gccttcctcc	gttgttgcgt	gagaacccgt	gtgcccccttc	3540
ccaccatatc	caccctcgct	ccatcttga	actcaaacac	gaggaactaa	ctgcaccctg	3600
gtcctctccc	cagtccccag	ttcaccctcc	atccctcacc	ttcctccact	ctaaggata	3660
tcaacactgc	ccagcacagg	ggccctgaat	ttatgtggtt	tttatacatt	tttaataag	3720
atgcacttta	tgtcattttt	taataaaagtc	tgaagaatta	ctgttt		3766

<210> 4
<211> 837
<212> PRT
<213> Human

<400> 4

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro	Trp
					5				10					15	
Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu							
								20		25				30	
Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	Pro	Arg	Ile
								35		40				45	
Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu	Arg	Phe	Glu	Ala
						50		55		60					
Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu	Ser	Arg	Asp	Gly	Arg
						65		70		75					80
Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu	Phe	Ala	Leu	Ser	Ser	Asn
						85		90						95	
Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr	Gln	Glu	Leu	Leu	Trp	Gly	Ala
						100		105						110	
Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys	Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln
						115		120						125	
Arg	Asp	Cys	Gln	Asn	Tyr	Ile	Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser
						130		135		140					
His	Leu	Phe	Thr	Cys	Gly	Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr
						145		150		155					160
Ile	Asn	Met	Glu	Asn	Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val
						165		170						175	
Leu	Leu	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys
						180		185						190	
Ser	Thr	Ala	Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ile

195	200	205
Ser Phe Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg		
210	215	220
Pro Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe		
225	230	235
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly Asp		
245	250	255
Asp Asp Lys Ile Tyr Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu		
260	265	270
Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile Cys Lys Gly		
275	280	285
Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp Thr Ser Phe Leu		
290	295	300
Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn		
305	310	315
Val Leu Gln Asp Val Phe Thr Leu Ser Pro Ser Pro Gln Asp Trp Arg		
325	330	